

M. PAK

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ENTERED ¹⁶⁴⁶ #9

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/254,590

DATE: 11/16/2000
TIME: 11:52:00

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NOV 28 2000

Input Set : A:\142107-3.app
Output Set : N:\CRF3\11162000\I254590.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Adelman, John P.
7 Maylie, James
8 Bond, Chris T.
9 Silvia, Christopher P.
11 (ii) TITLE OF INVENTION: Small and Intermediate Conductance,
12 Calcium-Activated Potassium Channels and Uses Thereof
14 (iii) NUMBER OF SEQUENCES: 48
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Townsend and Townsend and Crew LLP
18 (B) STREET: Two Embarcadero Center, Eighth Floor
19 (C) CITY: San Francisco
20 (D) STATE: California
21 (E) COUNTRY: USA
22 (F) ZIP: 94111-3834
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30 (vi) CURRENT APPLICATION DATA:
C--> 31 (A) APPLICATION NUMBER: US/09/254,590
C--> 32 (B) FILING DATE: 10-Mar-1999
33 (C) CLASSIFICATION:
47 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: US 60/026,451
37 (B) FILING DATE: 11-SEP-1996
40 (A) APPLICATION NUMBER: US 60/040,052
41 (B) FILING DATE: 07-MAR-1997
44 (A) APPLICATION NUMBER: US 60/045,233
45 (B) FILING DATE: 17-APR-1997
48 (A) APPLICATION NUMBER: WO PCT/US97/16033
49 (B) FILING DATE: 10-SEP-1997
51 (viii) ATTORNEY/AGENT INFORMATION:
52 (A) NAME: Weber, Kenneth A.
53 (B) REGISTRATION NUMBER: 31,677
54 (C) REFERENCE/DOCKET NUMBER: 014210-000730US
56 (ix) TELECOMMUNICATION INFORMATION:
57 (A) TELEPHONE: (415) 576-0200
58 (B) TELEFAX: (415) 576-0300
61 (2) INFORMATION FOR SEQ ID NO: 1:
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 561 amino acids
65 (B) TYPE: amino acid
66 (C) STRANDEDNESS:
67 (D) TOPOLOGY: linear

TECH CENTER 1600, 300

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69 (ii) MOLECULE TYPE: protein
72 (ix) FEATURE:
73 (A) NAME/KEY: Protein
74 (B) LOCATION: 1..561
75 (D) OTHER INFORMATION: /note= "human small conductance,
76 calcium-activated potassium channel
77 protein 1 (hSK1)"
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
82 Met Pro Gly Pro Arg Ala Ala Cys Ser Glu Pro Asn Pro Cys Thr Gln
83 1 5 10 15
85 Val Val Met Asn Ser His Ser Tyr Asn Gly Ser Val Gly Arg Pro Leu
86 20 25 30
88 Gly Ser Gly Pro Gly Ala Leu Gly Arg Asp Pro Pro Asp Pro Glu Ala
89 35 40 45
91 Gly His Pro Pro Gln Pro Pro His Ser Pro Gly Leu Gln Val Val Val
92 50 55 60
94 Ala Lys Ser Glu Pro Ala Arg Pro Ser Pro Gly Ser Pro Arg Gly Gln
95 65 70 75 80
97 Pro Gln Asp Gln Asp Asp Asp Glu Asp Asp Glu Glu Asp Glu Ala Gly
98 85 90 95
100 Arg Gln Arg Ala Ser Gly Lys Pro Ser Asn Val Gly His Arg Leu Gly
101 100 105 110
103 His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala
104 115 120 125
106 Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Thr Glu Thr Glu
107 130 135 140
109 Leu Ser Trp Gly Val Tyr Thr Lys Glu Ser Leu Tyr Ser Phe Ala Leu
110 145 150 155 160
112 Lys Cys Leu Ile Ser Leu Ser Thr Ala Ile Leu Leu Gly Leu Val Val
113 165 170 175
115 Leu Tyr His Ala Arg Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala
116 180 185 190
118 Asp Asp Trp Arg Ile Ala Met Thr Cys Glu Arg Val Phe Leu Ile Ser
119 195 200 205
121 Leu Glu Leu Ala Val Cys Ala Ile His Pro Val Pro Gly His Tyr Arg
122 210 215 220
124 Phe Thr Trp Thr Ala Arg Leu Ala Phe Thr Tyr Ala Pro Ser Val Ala
125 225 230 235 240
127 Glu Ala Asp Val Asp Val Leu Leu Ser Ile Pro Met Phe Leu Arg Leu
128 245 250 255
130 Tyr Leu Leu Gly Arg Val Met Leu Leu His Ser Lys Ile Phe Thr Asp
131 260 265 270
133 Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Thr Phe Asn Thr
134 275 280 285
136 Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu
137 290 295 300
139 Leu Val Phe Ser Ile Ser Ser Trp Ile Ile Ala Ala Trp Thr Val Arg
140 305 310 315 320
142 Val Cys Glu Arg Tyr His Asp Lys Gln Glu Val Thr Ser Asn Phe Leu

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143           325           330           335
145 Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly
146           340           345           350
148 Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr
149           355           360           365
151 Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala
152           370           375           380
154 Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met
155           385           390           395
157 Met Asp Thr Gln Leu Thr Lys Arg Val Lys Asn Ala Ala Ala Asn Val
158           405           410           415
160 Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Arg Leu Val Lys Lys
161           420           425           430
163 Pro Asp Gln Ala Arg Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala
164           435           440           445
166 Ile His Gln Ala Gln Lys Leu Arg Ser Val Lys Ile Glu Gln Gly Lys
167           450           455           460
169 Leu Asn Asp Gln Ala Asn Thr Leu Thr Asp Leu Ala Lys Thr Gln Thr
170           465           470           475
172 Val Met Tyr Asp Leu Val Ser Glu Leu His Ala Gln His Glu Glu Leu
173           485           490           495
175 Glu Ala Arg Leu Ala Thr Leu Glu Ser Arg Leu Asp Ala Leu Gly Ala
176           500           505           510
178 Ser Leu Gln Ala Leu Pro Gly Leu Ile Ala Gln Ala Ile Arg Pro Pro
179           515           520           525
181 Pro Pro Pro Leu Pro Pro Arg Pro Gly Pro Gly Pro Gln Asp Gln Ala
182           530           535           540
184 Ala Arg Ser Ser Pro Cys Arg Trp Thr Pro Val Ala Pro Ser Asp Cys
185           545           550           555
187 Gly
190 (2) INFORMATION FOR SEQ ID NO: 2:
192 (i) SEQUENCE CHARACTERISTICS:
193 (A) LENGTH: 580 amino acids
194 (B) TYPE: amino acid
195 (C) STRANDEDNESS:
196 (D) TOPOLOGY: linear
198 (ii) MOLECULE TYPE: protein
201 (ix) FEATURE:
202 (A) NAME/KEY: Protein
203 (B) LOCATION: 1..580
204 (D) OTHER INFORMATION: /note= "rat small conductance,
205 calcium-activated potassium channel
206 protein 2 (rSK2)"
208 (ix) FEATURE:
209 (A) NAME/KEY: Region
210 (B) LOCATION: 135..462
211 (D) OTHER INFORMATION: /note= "core region of rSK2"
214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
216 Met Ser Ser Cys Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn

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217      1      5      10      15
219  Leu Ser Ser Ser Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln
220      20      25      30
222  Pro Leu Gln Pro Pro Ala Ser Val Val Gly Gly Gly Gly Ala Ser
223      35      40      45
225  Ser Pro Ser Ala Ala Ala Ala Ser Ser Ser Ala Pro Glu Ile Val
226      50      55      60
228  Val Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala Leu Tyr Gly
229      65      70      75      80
231  Thr Gly Gly Gly Gly Ser Thr Gly Gly Gly Gly Gly Gly Gly Gly
232      85      90      95
234  Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly Thr Lys Ser Ser Lys
235      100      105      110
237  Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His Arg Ala Leu
238      115      120      125
240  Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu Ile Phe Gly Met
241      130      135      140
243  Phe Gly Ile Val Val Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala
244      145      150      155      160
246  Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu Lys Cys Leu Ile Ser
247      165      170      175
249  Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Val Tyr His Ala Arg
250      180      185      190
252  Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala Asp Asp Trp Arg Ile
253      195      200      205
255  Ala Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys Leu Glu Ile Leu Val
256      210      215      220
258  Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala
259      225      230      235      240
261  Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr Thr Ala Asp Val Asp
262      245      250      255
264  Ile Ile Leu Ser Ile Pro Met Phe Ile Arg Leu Tyr Leu Ile Ala Arg
265      260      265      270
267  Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser
268      275      280      285
270  Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe Val Met Lys
271      290      295      300
273  Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe Ser Ile
274      305      310      315      320
276  Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Ala Cys Glu Arg Tyr
277      325      330      335
279  His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp Leu
280      340      345      350
282  Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro Asn
283      355      360      365
285  Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly Ala
286      370      375      380
288  Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu Leu
289      385      390      395      400

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```

291 Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Thr Gln Leu
292                               405                               410                               415
294 Thr Lys Arg Val Lys Asn Ala Ala Asn Val Leu Arg Glu Thr Trp
295                               420                               425                               430
297 Leu Ile Tyr Lys Asn Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys
298                               435                               440                               445
298 Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg
300                               450                               455                               460
301 Ser Val Lys Met Glu Gln Arg Lys Leu Asn Asp Glu Ala Asn Thr Leu
303                               465                               470                               475                               480
304 Val Asp Leu Ala Lys Thr Gln Asn Ile Met Tyr Asp Met Ile Ser Asp
306                               485                               490                               495
307 Leu Asn Glu Arg Ser Glu Asp Phe Glu Lys Arg Ile Val Thr Leu Glu
309                               500                               505                               510
310 Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu
312                               515                               520                               525
313 Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp Phe Ile Glu Thr Gln
315                               530                               535                               540
316 Met Glu Asn Tyr Asp Lys His Val Thr Tyr Asn Ala Glu Arg Ser Arg
318                               545                               550                               555                               560
319 Ser Ser Ser Arg Arg Arg Ser Ser Ser Thr Ala Pro Pro Thr Ser
321                               565                               570                               575
322 Ser Glu Ser Ser
324                               580
325
328 (2) INFORMATION FOR SEQ ID NO: 3:
330 (i) SEQUENCE CHARACTERISTICS:
331 (A) LENGTH: 553 amino acids
332 (B) TYPE: amino acid
333 (C) STRANDEDNESS:
334 (D) TOPOLOGY: linear
336 (ii) MOLECULE TYPE: protein
339 (ix) FEATURE:
340 (A) NAME/KEY: Protein
341 (B) LOCATION: 1..553
342 (D) OTHER INFORMATION: /note= "N-terminally truncated form
343 of rat small conductance,
344 calcium-activated potassium channel
345 protein 3 (rSK3)"
348 (ix) FEATURE:
349 (A) NAME/KEY: Region
350 (B) LOCATION: 109..436
351 (D) OTHER INFORMATION: /note= "core region of rSK3"
354 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
356 Met Ser Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro Leu Ser Arg
357 1 5 10 15
359 Leu Ser Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Pro Glu Gly Gln
360 20 25 30
362 Pro Leu Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Ile Ile Ser
363 35 40 45

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VERIFICATION SUMMARY
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DATE: 11/16/2000
TIME: 11:52:01

Input Set : A:\142107-3.app
Output Set: N:\CRF3\11162000\I254590.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:579 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=[DNA]
L:611 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:627 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8, Value=[DNA]
L:643 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9, Value=[DNA]
L:659 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10, Value=[DNA]
L:675 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11, Value=[DNA]
L:691 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12, Value=[DNA]
L:1477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23, Value=[DNA]
L:1493 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24, Value=[DNA]
L:1509 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25, Value=[DNA]
L:1525 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26, Value=[DNA]
L:1874 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34, Value=[DNA]
L:1890 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35, Value=[DNA]
L:1906 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36, Value=[DNA]
L:1922 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37, Value=[DNA]
L:1938 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=38, Value=[DNA]
L:1954 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39, Value=[DNA]
L:1970 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40, Value=[DNA]
L:1986 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41, Value=[DNA]
L:2285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46